
APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

[illegible]

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGTTGCAGCCACACCCAGGACTGT
GTTGAAGGGTGTTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTG
TCTGAGAACCTTTACATTATAGATAGAGTAGTACATGGTGGATAACTCTACTCTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACAGTAAGACACCTGAAGGAGTATGTG
CTCCTATTATTCTGGCTTTGTGCTCTGCCCCAACCCCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTCCAACAGAGGCCAAGACCCATTTTTCCTA
TTTGATCTGTTTCCAATGTGTCATTGGATGTCAGTGCTATTCCAGAGTTGTACATTGTCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATATCGAATGCTTGATGTCT
AAAACATAAAAAATTAGGAAATCAAGAAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCTCTGACAACAACAGCTAACGAATTCACCAAGATTCACCAAAAGCCTTTCTAACCAAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAACCACTAACTAAGTGAAATACCACTTAATCTTCCCAAT
CATTAGCAGAACTCAGAAATCATGAAAAATGAAGTTAAGAAAAATACAAAAGGACATCAATCAA
GGAATGAATGCTTTACAGTTTGGAAATGAGTGCAAAACCCTCTTGATAATAATGGGATAGA
CGCAGGCGCATTTGAAGGGGTGACGGGTTCATATCAGAAATGCGAAGCAAAAACTGACCT
CAGTTCCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTACAAGGCTGGCGTAGGAAACAA
CAAAATCACAGATATCGAAAAATGGGATCTTGCTAACATACCCAGTGTGAGAGAAATACATT
TGGAAAAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTCTCTGTCCAACAGTGC
AAAGATGAAGAAATCTTTATACAGTGCATAAAGTTTATTCAACACCCGGTGAAATATCTGGG
AAATGCAACCTTGCAACATTTCTGTTGTGTTTGGACAGAAATGAGTGTTCAGCTTGGGAACCTT
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TGGAACTACTGCAACTCTATTAAATAATGGTAGTATTATATACAGCAAAATATCTATTCTCA
AGTGGTAAGTCCCACTGACTTATTTATGACAAAGAAATTTCAACCGAAATTTGGCCAAACTATT
GATACATATAAGGGGTGAGAGAAACAAGCATCTATTGCGAGTTTCCTTTGTGGTACAATGAT
CTTACATAAATCTCATGCTTGACCAATTCCTTTCTTTCATAACAAAAAGTAGAATATTTCGCT
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TAGCAAAATTTGTGCTCTTTCAATTGTGCTGTGAGAAAAACAGAAATTAACAAAGACAGTAATGT
GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACCTTGGGTAGTACTGTAAATATTTTAAAT
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TAAATGCTACTCTAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTTAATTATT
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TTCAACTCTAAGGAATATTTTGTAGATATCCCTTTGGAAGACCTTGCTTTGGAAGAGCCTGGA
CACTAACAAATTTACACCAAAATGTCTCTTCAAATACGTATGGACTGGATTAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAAATTAACAGACAGAAACCAAGGCTCTA
TATAAATGCTCAGAGTCTTTATGTAATTTCTTATTGGCATTCACATATGTAAAAATCAGAAA
ACAGGGAATTTTCATTAATAAATATTGGTTTGAAT

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	CLASS	SUBCLASS

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1

<MW: 43302, pI: 7.30, NX(S/T): 1

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YNKISTVELEDFKRYKELQRLGLGNKITDIENGLANI PRVREIHLNNKLLKKIPSGLP

KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV

QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

[illegible]

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

[illegible]

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

[illegible]

100

FIGURE 5

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

GCGGACGAGCCCTAGCCGCCACCGTCGCTCTCGAGCTCTCGTCGCCACTGCCACGCCGCCGCCGCTCACTGCG
TCTTGGCTCTCGGCTCTCCGCGCTCTCCGCCGGGCAATGCGAGCCCGCGGCCACGGCGCCGGTGCAGCATGCG
TCTGCGCGCTGCGCCTGTGCTGTCTGCTGCTGCGAGGGCGGCCGAGGACGACTCTCGGCCAACCGCGCGCG
CGCGCGCTCTTGTGCGCCCGGCCCTGCGCGCGAGCCCTCTGCGGAAATGGGGGTGTGTGCACATCTCGCCCTCTG
AGCGGACCGCGAGCAGCCAGCGCCCGCCCGCGGCGAGCTGCGTCACTGACGACTGCCCGCCGGGATCTCGCGG
CCAACTGCGACGTTTGTGCAGATCTCTTGTGCCAGCAACCCCTGTACCATTGGCAACTGCAGCAGCAGCAGCAGCA
CGACGACGAGTGTGCTCATCTGTCATTTGAATGAAGAGCTTGAAGGCTCCCAACTGTGAACAGGCATCTCCAGCT
TCCGAGCACTGCTGCGAGCAGCAATCATGCGACCCCGACAGCTTACGCTGTCTTGTGCTACTCAGGAGCCTGACA
AAATCTCGCTCGCTCTGCTACGGCAACGCTGACACTGCTACCTCGGACCGGAAACAGGCGAGAAGGTTGTAGAAA
CTGTAATGGGATCAAGTGGAGGTGATCTCCAGATATTGCTTGGGGAATGCGAGTTCAACGCTTCTCGGGTGGCC
GCTTGATATCTCTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCGGCAAGATGCGACTGCTCATGATTTTGT
TCTGGAAGTCAAGCGCAAGATTTCCAACAGTCTGCCCTCATAGATGAGACAGATGTGACCTGCTTGGTGAATGATTCT
CAGGGGAGCTGGTCTCTCTGAGGAGATGCTCGCTCTGGGGAATAACTCTTTATTGGTTTGTGAATGATTCT
TGACTTAAGTCTATTGTGGCTTTGGCGTTAACTCTGGTGGTGAAGTGCAGCACTGTGCTGCCGGGGAGAGTCA
CAAGTACTTGGAGTGTTCAGGAAAGGAAATGACACAGGAACCGCTCAGGAGCAAGTTTCTGTACTGTG
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GTATTGATGCAAAATGAAAGCAAGATGGGAGCAATTCACCTGCTTTGGCTCTCTGTGTTATATCTGAGAGAGCTT
GCCAGTCCAAGATTGATTACGTGCTCTAGACCAATGCGAATAATGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCGCAGTGTCCAGAAAGATACATTCGGATCTGCTTTGTGAAGAAAGGTGAGCCCTGCGCTCTGCTCTG
GCAAGCAACAGGCACTGCTATCTGTGACCGGGATCACTTTACCTGCAATGCAGGCCCGGCTTCCACGGSCCGA
CCTGTGCCCAGCTATTGATCTCTGTGCGCTCAGCCCTGTGCTCATGCGACGCTGCCGACGCTGGGACACAGCT
ACAAATGCTCTGTGATCAGGTTACCATGCTCTACTGTGAGGAGGAATAATAGATGCTCTCCGCTCCAT
CGCTGAATGCGAGCCACCTGACGGGACCTCGTTAATGGCTATGATGTGTGTGCTGCCGACATCAAGGACCT
CTGCTGAAATTTACAAAGATCTCCGCGCTAACCTCAGCTCTGCTTACGATTAATGCAATGCTGACCACTGCG
ATGCGACGTGCTATCTGTGCAACCGGTTTACAGTGAAGAGTGCACATTGACATAAATGAATGTGTGAGTAACC
CTCGCCACATGTGGGAGAGCTCGTGGACAGCCCAATGGTTTACATGBCATGCTCCCGCGCATTTGGGTTGGG
CAAACTGTGAGATCCCACTCAAATGGAATCGGGACATGCGGAGAGCTTCAACAAATGCGCAGGCACTCCC
TCTCATCATCATTTGAGCGCTCTGCTGTGCGCTTCACTCTATGCTGATCATCTGATGTGGGAGTTTGGCGCA
TCAGCGCCATTGAATACACGGGTTCTCCAGCGCTCAGCTATGAGGAGTTCTACAGTCCGCGAGATCGACAGCG
AGTTTCAGCAATGCTGATTCATCCCGCATGCGAGTTTGGAAAGAAATCCGCGCTGCAATGTATGATGTGTA
GCCCATCGCTCGCTAGAAGATTACAGTCTGATGACAAACCCCTGGTCACTGATTAATCAAGATTGTGTAAT
CTTTTGTGTGATTATTTTCAAAGAGATGAGATACACTACATTTAAATATTTTAAAGAAATAAAGAGCTAA
GAAATTTAAATGCTAGTCTCGCTCAAGAGTTTTCAGTAGAATATTAAGAACTAATTTCTGCGAGCTTTAGTTGT
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GAATAAGTCTAATCAAGAGAAAGTTTCTGTTTGTGACGTTTGAATGATTTTAAATGATTTTAAATGATTTTAAATG
GTAACTGATGATGATGATATAATAGAGATTACCCGTTACTTAAAGAAAGTCTGAATGTTCGTTTGTGGAAA
AGAACTAGTTAAATTTACTATTCTCAACCCGAATGAATTAGCTTTGCCATTTCTGTCATGCTGGGTGAATTAAC
TTATTTCTGCACTGTTTGTGTGAATTTTGTGGAACCTCTAGATGCTTTTCGAGTTTGTGTTTGTCTATTTTGTG
TCGAACTAGGCCTCAAAACATCACTGTAAGAAAGGCTTACGAGGCAAACTCGATTTGTTTGAATCTATATT
TTCTTTTAAAGAGCTCAAGGGTCTCATATTTGTGAGTAATTTTACATTTGATTTGTTTGTGCTCAAGGGTAG
TAAATGTAAAGAGATGATGGTCTCTTCACTAGTAGATTTCTCATAGTCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGATTTGATTTGATATGTGCTTCTCTGATTTCTGCTAATTTCCAACCATTTGAATAAATGTGATC
AAGTCA

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

[illegible]

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSTCTPAGISGANQQLVADPCASNCHHGNCSSSSSSSSDGYLCICN
EGYEGPNCQEIPALPSLATWSTESMAPRQLQVPADQPEPDKILPRSQAATVTLTWPQKTGQK
VEMKWDQVEIPLDIACGNASSNESAGGRVLSFEVPQNTSVKIRQDATALILLWKVATGFG
QCSLIDGRSVTPLQASGGLVLEEMALGNNHFIGFVNDSVTKSIVALRCLTLVVKVCTSCVPG
ESHANDLECSGKGKCTLPKPEASTFSTCEBQYVGTFCBEYDACQRKPCQNNASIDANEKQD
GSNFTCVCLPFGYTGELCQSKIDYCLIDPCRNAGTCISSLGGTFCCQCEPGYFGSACEEKVDP
ASSPCCQNGTGYVDGVHFTCNCSPGTGTPTCAQLIDFCALSPCAHGTCRSVGTSYKCLDPC
YHGLYCEEYNECLSAPLNAATCRDLINEDVGYECVCLAEYKGTGHCELYKDCPANVCSLNGATC
DSDGLNGMTCICAPGFTGEEDICDNLDSNPHCHGGSGCLDPNGYCNCPHGWANGCEIHL
QWSKSHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICISRISEYQGSSRPAYEEFYN
CRSISEFSNAIASIRHARFGKKS RPAMYDVSPAIYEDYSPDDKPLVTLITKDL

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

APPROVED BY TWIFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCCTCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAAATGCACCACGAAGCCGTGAGAGCAACTTTTCTGTACTGTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

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FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAAC
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

APPROVED BY CHARTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

REF ID: A507600

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCCATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGTTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
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TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGTGTGTGCAACAGTGTCTCGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTGATGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAACCTGCTGCGGGTCTT CAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCTTGGAGGACAAGTTCCCGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACCATGGCCCCAG
TCCTTGCAAGTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCCAAAAGTTCCCCTGTTGTGCAGGCACA
AATATTCTCTGAAATAAATGTTTGGACATAG

APPROVED BY	CLASS	SUBCLASS
	CONFIDENTIAL	

TOP SECRET

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

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TQKLACLIGVEGGHSLDNLISILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPNSANVSTVADHFHDIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPKAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

ALPHA	CLASS	SUBCLASS
BY	CLASS	SUBCLASS
REACTIVITY		

TOEEN = 2500000

BY	CLASS	SUBCLASS
CHARTERMAN		

AAAACCTATAAATATTCCGGATTATTACATACCGTCCCAACTCGGGCGGGATCCGCGGCCG
 CGAATTTCTAAACCAACTCGCGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
 CCCAGGGCTGCTCAAGAGCAGGCACGGGCCCTGATCGGGGACTTCCCGCTCGTGAGCGGCCAC
 AACGACCTGCCCTGGTCTCTAAGGCAGGTTTACAGAAAGGGCTACAGGATGTTAACTTCGC
 CACTTTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
 TCTGGTTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
 CAGATTGACCTCATA CGCCGCATGTGTGCCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
 TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
 TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
 ACCCACACCTGCAACACACCCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
 CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCTGGGCA
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
 GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGCTCTCGGAATGTTC
 TGATGACATCCTGCACTTCTGAAGAAGAACGGTGGCGCTGTGTCGAGATCACTTCGACCATC
 GAGTAATACAGTGCAACCCATCAGCCAAATGTGTCACCTGTGTGGAGATATGATGGGGCCGCAAAAT
 AAGGCTGTCAATTGGATCCAAGTTCATCCGGATTCTGTGGAGATATGATGGGGCCGCAAAAT
 CCTCAGGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCGTG
 GCTGGAGTGGAGAAGAGCTTTCAGGGTGTCTCTGTGGAACCTGTGTCGGGTCTTCAGACAA
 GTGGAAGAGGATCAGGAAGAAAAAACTGGCAAAGCCCTTGGAGGACAAGTTCCTCGGATGA
 CGAGCTGAGCAGTTCCTGCCACTCCGACCTCTCAGTCTGCGTCAGAGACAGAGTCTGACTT
 CAGGCCAGGAACCTACTGAGATTTCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
 GTCTCAGAGTCTCCCCCCCCCTGACAAAACCTACACATGCCACCCTGCCAGCACCTGA
 ACTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACCC

CLASS SUBCLASS

><subunit 1 of 1, 446 aa, 0 stop

><NX (S/T) : 5

><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRLDGLVGAQFWSAYVPCQTDRLDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMVDSLHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPPDILQ
LLKKNGGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIFIGGDDYGAGKFPQGLE
DVSTPYPLVEELLRSRGWSEEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIP IHWTAKLPAKWSVSESSPHDPKTHTCPPELPGGP
SVFLFPKPKDT

[illegible]

FIGURE 13

[illegible]

APPROVED BY	O.G. FIG.	
	CLASS	SUBCLASS
DRAFTSMAN		

0 9 0 1 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 103

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRGPAAQSARRPPPLLLLLLVCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLLPELSRVLNASTLALALANLNGSRQSRGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLWYQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTDDPPDVHVS RVGG
LEDQLSVRWVSPPALKDFLQAKYQIRYRVESVDWKVVDDVSNQTSCLAGLKP GTVYFVQ
VRCNPFGIYGSKAGIWEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGFPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

APPROVED	CLASS	SUGGEST
BY	DATE	
CHARTMAN		

100-250000-100

FIGURE 15

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACCAAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCTCTCGTGAAGCTTTTATTCCCTAA
 GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTCTCTGGGATATAAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTTGTCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTGACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTGCTGTTGGA
 TTTTCATAAACTTTGACAGATGAAGTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGTCTTAATTTTCGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTTATTCCATCTTCTATAGCTTTTTTAAACACATTGAAAAGGATCCTTCTGAGCGTTT
 CCTGGCAGTTTTAAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATAGCACCTAGTTTTCTGAAAAGTATTTACCAGGTTTAGTTGATGTCTATCA
 ATAGTGCCAGAATTTTAAATGTTTGAAGTCTGTTTTTCTAATTATCCCCATTTCTTCAATA
 TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
 CCAAAATGACTTTATTAAAAATAATTTCCAAGATTATTGTGGCTCACCTGAAGGCTTTGCAA
 AATTTGTACCATAACCGTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT
 ATAATTTGTGTTTCTTTTTCTGTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAAGTCTCAATGGGTAGGTTTC
 ATCTTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
 AA
 AA

APPROVED BY	O.G.F.G.	SUBCLASS
BY	CLASS	
DRAFTSMAN		

100-251160

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVFPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRMLH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216



FIGURE 17

APPROVED BY DRAFTSMAN	O.G. FIG.
	CLASS SUBCLASS

100-350100

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
 GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAGCGCGGGGGCTGGAGCACCACCAA
 CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
 GCGAGAGGACCCCGGCTCCGGGTCTCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
 TGCTCCTGGGCCTGGCGGCGGGTCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
 CCGGGGCACCCCGCCTTCCAGGCACGCGGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
 CGATGGCCGACGGCCGCGACGCGCGCGCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
 GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
 CCCACCGGGCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
 CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCTTGCCCTTCGACCGCGTGCTGGTGAACG
 AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
 TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
 ATCCATTGCCCTCTTCTTCCAGTTTTTCGGGGGTGGCCCAAGCAGCCTCGCTCTCGGGGG
 GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
 ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTTCTGGTGTACTCCGA
 CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
 TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCTCCAGGAGGGCTGGCCCCCTGGAATATT
 GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTGCTGCTGGCAAGGAATGGGAAC
 AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCCAAGACCA
 GAGGAGTGTGTGTGCTGGCAAGTGAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCCAGGT
 GGGGTGCTCTCTTCTGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGCTCCTGGG
 GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAA
 AAAAAAAAAAAAAA

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MRPLLVLALLLGLAAGSPPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP

GEKGEGGRPGLPGPRGDPGRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP

FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP

KPASLSSGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCTTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCTTGC GGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTGGCGTCCTTTGTGAAGTGGTGAG
CCTATGTTTTCAGAGGGGCGAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGGCAG
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCTACTCCCCGGAGGCCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCGGGAGGAGGAGTGTCTGCTGCTGTGACATCGGCTACGGGGAGGCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGACAGACATCCTCGCCTTCTATCTGGGCCG
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCCTTACCA
GTTTTCCTTTTGGGCAGCCTGACAACACCGGCTGGTGTGGCTGAGTGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTT
GAGGCCTGACCACATGGCTCCTCGCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTAAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTTCCACCTGGCCGAGAC
CCTGTGGGGCAGCGGAGCTTCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
ORGANIZATION		

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APPROVED	BY	CLASS	SUBCLASS
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CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCGCGCGGGTCCCCGAGCGTCCCGCGCCCTCGCCCCGCCG**ATG**CTCCTGTGCTGTGGGGCTGTGCGCTGGGGCTGTCCCTGTGTGTGGGGTCGCA
GGAAGAGCGCGACAGCTGGGGCCACTCTTCGAGCAGGATGAGCATCAGGTCCTCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAACCAAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACCC
ATCATTTCCCGTTATGCGCTTCACTACGTTTTCCTGCAGAAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGAGATTTCAGCTGCAGCTTTCACTACCAACTTCACTATGCT
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAAGAGTGGTGATAGG
GTAAAAAGAGAAAAGGATAAAACACCAAGAGAAAAAGGAGAGAGGATGAAATTACAG
AGCTTCTCAGTGTATTCCGCAAGGACAAAGCGCCCTTTTCTGAGTTATGAGGAGCTTC
TGCAGAGCGCCTGGGCAAGTACGACACAGCATCAGCGTCGGCGCCACGAGCCTGTCGGGG
AGGCTTGAGCGTGGACGTGAATATCTGGAGAGCGCGGCATCGATCCTGGAGGTCTGCGC
GCTTACAACAGCAGGACAGAGGGGCGAGTGGGCGCGGGGAAGTGAATTCTGGGCTCCCCCAT
CTACTGTCAATTAAACCAATTGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAAAATGGAATTTTGGAGACATTATCACTAGATATGACGTCAATAG
AAGACCTTCTCTTTTACCACCAAGATGTGTTATCTGCTGTGACAGATGCTTGTCTCTTA
GGAACCAAATCCGGGACCAAGATGAGTCCCTTTCACAAATTCTCCATGACCTCCGACCCCA
GGAACGTTTCAGTATCATTTGGAATTTTCCAACCGGATCAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCGACAGCATCAGGATGGGAAAGTGATCATCACATATGTCAACCATGTCAGCTTGG
GGCACACATCAACGGGGCCCTGACAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGGCCCA
CAGTGGCATTTGGAGACCGGAGCGTGTCCCTTCAGTCTTCTTCGACGGATGGGAAGCCACGG
TCGGGGAGAGCGACCTCTCAAGATCTCAACAACACCGGAGAGGCGCCCGAGGGCCAAAGT
TGCATCTTCAACATTGGCATCGGCAACAGCTGGACTTTCAGGCTGTGGAGAACTGTGCTGT
GGAGAACTGTGGCTCACACGGGCGGTGACGAGGAGGAGACGAGGCTCGACGTCACTCG
GGTTTTCAGATGAATCAGGACCCCGCTCTCTCTGACATCCGCATCGATTCCCCCAGC
TCAGTGTGTGACGGCCACAACAGCCCTGTTCCTCAACTACTTCAACGGCTCGGAGATCATCAT
TGGCGGGAAGCTGTGTGACGAGGAAGTGTGATCACTGCAGCTGGAGGTACCGCGGACAACA
GTAAAGAAATTCATCATCTGAAGACAGATGTGCTCTGTGCGGCTCAGAAGGACGGGAAGAT
GTCAACGGAAGCCCGAGGCTGGAGGCGATGGAGAGGGGACACCAACCATCGAGGCTCT
CTGGAGTACCTCACCACAAGAGGCTGCTGAGTCTTGGCTGCAAGTGACGATGAACCGG
AGAAGGAGCGCTCGGCGACGGGCGCCAGGCGCTGGCTGTGAGCTACCGCTTCTCACTCTT
TTCACTCCGTGAAGCTGAGGGGGCCGTCCACAGCTGATGAGTGGAGAGGACCCACG
CATGTGCGCTGCGATTGGGACCCGAAACCGGTGGTGCAGAGCGTGCAGGAGGCTGGCAGCGAC
CAGGACACTTGTCTCAAGAAGCCAACTCCGTCAAAAAAAAACAAAAACAAAAAAGA
CATGGGAGATGTGTTTTCCTCTCCACACCTGGGATACGAT**TGA**GAGATGGCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGCTGGCACCTTGATCTTGACCTC
CCAGCCTCCAGAAGTGTGAGAAATAAATGTGTTTGTAAAGCTAAAAAAAACAAAAA
AAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLKTKPLMTFEFSVKSTIIS
RYAFTTVSCRMNLRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDGGPPSTVINQNETFANIIFKPTVVQQR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIIGFSNRKIVWKDHLISVTPDSIRDGKVIYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPRPQKAGKDV TG
SPRPGDGEGDNTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGFPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGTGCCGAGCGGATCCCAAGTGTGCGG
GGCAGCGGCGGCGGCGGCGCCTCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCGCGG
CACTGATCCCCACAGGTGATTGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCCTTGAAGGACAGCAGGTTTCAGT
TGCTGAA'TTTTCTAGCAGTGAAC TCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGCTCCCAACCAGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCAC TGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTGAGACATGTACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAAGTGATCTGCCAGCTGG
AGCACCTTGGGTCACTGGA AACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCT
CAAGTGACATTCAGATGACTTATCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAAATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGCGTAACTTCTGAGAGTGCATG
ATGAAATGCCTCAACACGCGTACTGTCTGGGCCCAACTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAGGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACCAACTATCCCTCTCCCAACAACACCACCACCA
CCACCACCACCAACGACCATCTTACCATCATCAGATTCCCGAGCAGGTGAAGAAGG
TCGATCAGGCGAGTGCATATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTTCGCCAT
CTGTGTGCTGTGCTCATCATTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCACTATAGATCAGCCTTTTGTGTTCAAT
GAGGTGTCCAAC TGGCCCTATTTTAGATGATAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518

<subunit 1 of 1, 440 aa, 1 stop

<MW: 48240, pI: 4.93, NX(S/T): 7

MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTLKG
KSEVEEWSMDYTVTSQMLMKVHKEDDGVPVICQVEHPAVTGNLQTRYLEVQYKQVHIQMT
YPLQGLTREGDALELTCEAIGKQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

APPROVED	OG FIG.	SUBCLASS
BY	CLASS	
DRAFTSMAN		

TOP SECRET

FIGURE 25

APPROVED BY DRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA
 CCGGCCAGGAAAGACTGAGGCCGCGGCTGCCCCGCGCGGCTCCCTGCGCGCGCGCGCGCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCGCGCTGCTCTGTACTTGGCCCT
 GGGGCTCGGGGTGCGAGGGTCCCCATCCGGCTGCCAGTGACGACGCCACAGACAGTCTTCT
 GCACTGCCCGCCAGGGGACCAGGTCGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
 GTCTTTGAGAACCGCATACCATGCTCGACGCAAGCAGCTTTGCCGGCTGCCGGGCTGTGA
 GCTCCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGCTGCTGCTGTGG
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGATCCTGGACACTGCCAACGTGGAG
 GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTACGCCGCTTGG
 CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACCCGATTGCCAGCTGCGGCC
 GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGACGGC
 CCTGCCTGGCGACCTCTCGGGCTCTTCCCCGCTGCGGCTGTGGCAGCTGCCCGCAACC
 CCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCTGGGTGCGGAGACACGTCA
 CTGGCCAGCCTGAGGAGCGCGCTGCCACTTCCCCGCCAAGAACCTGGCCGGCTGCTCCT
 GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACCTACGACGCCACAGTGCCCA
 CGAGGCCGTGGTGGGGAGGCCACAGCCTTGTCTTACTGCTTGCTCTACTGCTGTAGC
 CCCACAGCGCCGCCACTGAGGCCCGCCAGCCCGCTTCACTGCCCCACCGACTGTAGGGC
 TGTCCCCCAGCCCGAGGATGCCACCGTCCACCTGCTCAATGGGGGCACATGCCACCTGG
 GGACACGGCACCACTGGCGTGTGTGTGCCCCGAAGGCTTACGGGCTGTACTGTGAGAGC
 CAGATGGGGCAGGGGACAGGCCACAGCCCTACACCGATCACGCCAGGCCACACGGTCCCT
 GACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGTACCTCC
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGCCCTGT
 AAGCGGCTGTGTGAGCTGCGACTGCTGCTGCTGCTGAGTACACGGTACCCAGCTGGG-
 GCCCCACGCCACTTACTCCGTCTGTGTCTGCTTTGGGGCCGGGGCGGGTCCCGAGGGCG
 AGGAGGCTGCGGGGAGGCCATACACCCAGCGTCCACTCCAACACGCCCCAGTACC
 CAGGCCCGCAGGGCAACCTGCGCTCCTCATTTGCCCGCCCTGCGCGCGGTGCTCCTGGG
 CGCGTGGCTGCGGTGGGGGAGCCCTACTGTGTGCGGGGGGGCGGCCATGGCAGCAGCGG
 CTGAGGACAAGGGCAGGTGGGGCAGGGGCTGGGGCCCTGGAACTGGAGGGAGTGAAGTGC
 CCCTTGGAGCGACGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGCTGA
 GTGTGAGTGGCCACTCATGGGCTTCCAGGGCTTGGCCCTCAGTCAACCTCCACGCAAGC
 CCTACATTAAGGCCAGAGAGAGACAGGGCAGCTGGGGCGGGCTCTCAGCCAGTGAGATGGC
 CAGCCCCCTCTGCTGCCACACCGTAAAGTTCTCAGTCCCAACCTCGGGGATGTGTGAGA
 CAGGGCTGTGTGACCACAGCTGGGCCGTTCCTCTGGAACCTCGGTCTCCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCATGAGGACAGTGT
 CCGCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
 GCATGCTGGGCCCTGCTGGGCTCTCCCACTCCAGCGGAGCCCTGGGGCCAGTGAAGGAAG
 CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTTAGTCTTGGCCCCAGG
 AAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTAGGAACATGTTTGTCTTTTAA
 AATATATATATATTTATAAGAGATCCTTTCCATTTATCTGGGAAGATGTTTTCACAACTC
 AGAGACAAGGACTTTGGTTTTTGTGAAGACAACGATGATATGAAGGCTTTTGTGAAGAAAAA
 ATAAAAAAAAAAAA

10450" 2541160

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLLP LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P D T V G L Y V F E N
G I T M L D A S S F A G L P G L Q L L D L S Q N Q I A S L R L P R L L L D L S H N S L L A L E P G I L D T A N V E A L R L
A G L G L Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L A
G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P
E E T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P
A T E A P S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q
G T R P S P T P V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V
T L R L P A S L A E Y T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E
G N L P L L I A P A L A A V L L A A L A A V G A A Y C V R R G R A M A A A Q D K G Q V G P G A G P L E L E G V K V P L E P
G P K A T E G G E A L P S G S E C E V P L M G F P G P G L Q S P L H A K P Y I

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

APPROVED	OG FIG	SUBCLASS
BY	CLASS	
INRAFTSMAN		

101000-2501160

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTTACCCGCCCCGCCACC
 TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
 ATCTCCTTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
 CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
 ATGGCTCTGCTGACCCAACAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
 GGGGACAGGAGGCCCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA
 GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
 ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCTATTAACGCCACCTCCAA
 GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
 AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGT
 CTGTTTCAAGACGTGACTTTCACCATGGGTGAGGTGGTGTCTCGAGAAGGCCAAGGAAGCA
 GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGACCGGGCTACAAACAGCT
 GCTATAGCGCAGGTGTCTTCCATTACACCAAGGGGATATTCTGAGTGTATAATTCCCCGG
 GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTTGTGAAACTGTGATT
 GTGTTATAAAAAGTGGCTCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
 GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
 CCCGTTCTCACTTTTCCCTTTTCATTCACCCCTTAGACTTTGATTTTACGGATATCTTG
 CTTCTGTTCCCCATGGAGCTCCG

101280-2501100

BY	CLASS	SUBJECT
CONFIDENTIAL		

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

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SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHVPIN
ATSKDDSDVTEVMWQFALRRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

APPROVED BY CRAFTSMAN	O.G. FIG.	SUBCLASS
	CLASS	

101000-25011000

FIGURE 29

CACTTTCTCCCTCTCTCTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCGAGAGAC
 CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA
 CCGCCCCCACCCTCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCTGCTCTGTT
 TCCTTCACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
 TGCTCTAGGGGGCGCGCGGGAGGAGCGCGCGGGGACGGAGGCCCGGAGGAAGATGGGC
 TCCCGTGGACAGGAGCTTCTGTGCGTACTGCTGCTCTTGCCTTTGGCTCTGGGCTGGT
 CCTGAGTCTGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCGCTCCGGACCATTCCGAGAGGGCTGAAGAAACAATAGAAATACAGGCCACACTCAG
 GACCAGGGGCTCCCTGCTTCCGGTGCTTGGCTGCTGTGACCCCGGTACCTCCATGTATCC
 GGCGACCGCCGTGCCAGATCAACATCACTATCTTGAAGGGGAGAGGGTGACCGCGGAG
 ATCGAGGCTCCAAGGGAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
 CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCG
 CTTTTCGTGGGCGGAAGAAGCCATGCACAGCAACCACTACTACCAGACGCTGATCTTGC
 ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTCTACTGTATC
 GTGCCCGGCTCTACTTCTTTCAGCCTCAACGTGCACACTGGAACACAGAAGGAGACCTACCT
 GCACATCATGAAGAAGGAGGAGGTGGTGTATCTGTTCCGCGAGGTGGGCGACCGAGCA
 TCTGCAAGCCAGAGCCTGTATGTGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCTC
 TACAAGGGCGAAGCTGAGAAGCCCATCTTACGCGAGGAGCTGGACACCTACATCACTTCAG
 TGGCTACCTGGTCAAGCAGCCACCGAGCCCTTAGCTGGCCGGCCACCTCTTCTCTCGCC
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC
 CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACAGAAAGCCAAAGCGATCGGTGCTCC
 CAGATCCCGCAGCCTCTGGAGAGAGTGCAGGAGATGAAATCACCAGGGCGGGGACCCCG
 GAGAACCCTCTGGGCGTCCGCGGCCCTCTCTGCACATCCTCAAGTGACCCCGCAGCGC
 GAGACGCGGTGGGCGCAGGGCGTCCAGGGTGCGGCACCGCGGCTCCAGTCTTGGAAATA
 ATTAGCAAAATCTAAAGGTCTCAAAGGAGCAAGTAAACCTGGAGGACAAAGAAAGGG
 TTGTTATTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCTTTTCACTTGAG
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGCCGGGCGAGG
 AAACACTCTTGGCTTAATCTTTTAAAGCCAGTAGGAACCTTTCTGAGGTACAGCTGCGAGGT
 CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCAGCTGCGAGGT
 GATGGGGGCTGGGGCCCGAGCGCTCAGCCTCCGAGGGGACAGCTGAGCCCTGCTTGGC
 TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA
 GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCTGTGGCCACCCAGAGCCCTGGGGGTGGTCTCCATGCTGCCACCCCTGGCATCGCTCC
 TTCTGTGCGCCTCCACACAAATCAGCCCCAGAGGCCCGGGGCTTGGCTTCTGTTTTT
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCTCGTGGGCTAAGCATCACCGCTT
 CCACGTGTGTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCTCCT
 CATCCAGGCTCTGACCACTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAG
 AGACCAGAGTCAAGAGGAAGTACAGTCCCAATCACCGGTGTGAGGATCACTCTCAGGAGC
 TGGGTGGCAGGAGAGGCAATAGCCCCGTGGCAATTCAGGACCAGCTGAGAGCAGGGTGGC
 GTGTCTCCAGGCTCTCTGCCCTGCCCATGGCCACCCAGACTGTATCTCCAGGAACCC
 ATAGCCCTCTCCACCTCACCCATGTTGATGCCAGGCTCACTCTGTGTAACCCCTGGGGC
 CCCAAACCCCGCTGCTCTCTTCTTCCCCCATCCCCCACTGGTTTTGACTAATCTG
 TTCCCTCTCTGGGCTGGCTGCCGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
 CTGCGGGTCACTCTGAAGCTGAGCGAGTTGCTGTGGGCGTCCCGGAAGCAGAGCGCCACACT
 GCTGCTTAAGCTCCCCAGCTCTTTCAGAAACATTAAACTCAGAATGTGTTTTCAA

APPROVED	DATE	CLASS	SUBCLASS
BY			
EMPLOYEE			

10-100-250146-6

APPROVED	O.G.P.D.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

RLYKGERENAI FSEELDTYIT FSGYLVKHATEP

amino acids 1-25

amino acids 93-97

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

amino acids 150-154

amino acids 104-107

BY	CLASS	SUBCLASS
	O.G. FIG.	

CGCGAGCATCCGCTGCGGTCCTCGCGAGACCCCGCGCGGATTGCGCGGTCCTTCCCGCGG
CGCGCAGCAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCGAGCCTTCTTAAAGCAAATCAGACGAGGGAGGATTAT
CCTTGTACCTTTGAAGACCAAAATCTAACTGAATTTAAATGTTCTTCGGGGGAGAGGGAG
CTTGACTTTACACTTTGGTATAATTTGCTTCTCGACACTAAGGCTGTCTGCTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTGTCATTGACATCCAGTCATCTCTTTCAAGGGAATC
AGAGCAATCATGAGCCGTATATACTTCAACTCAAGAAGATGCATTAATCTTGTGTTCAAC
AAAAACAATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCTGTCATTGAAACCCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCACCTTTGACAGAAATTTGCCAAG
CCAAGAGTTACCCAGGAAGATTCTCTCTACATGGCCAATTTTCAAGCAGTCACTCCCC
TGATCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTTGGATCTCTCATGACACTCGTGAGAAACTATTAAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCGTTCTCAGAGTTTCACAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAATGTGAGTGGCTCCAGCTCATCGGTGCGAGTTGCTTCTTCCA
CATACCACCTCGGCTACTTCAAAGCCCGCCACCTTCTACCCACCAATGCTTCGATGACACC
TTCTGGGACTTCCAGCCACAGCTGGCCACCAAGCTTCACTGTAAACCATGTCACTTCTC
AGGCTCCACAGACCTCATTTCTACAGTTTTTACACGGGCTGCGGTACACTCAAGCAATCT
GCTACAACAGCAGTTCTGACTACCACTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATACCGGTTTACAGAAATCTCAAATTTAACTTTGAACAGAGGAAATGTGTATAACCCTA
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACTGCTTCTCTGGGAAGT
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGCGAGTGTTCAGAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGTCCTGCTTCTTGGTGTCTGTTCTCTGGTGATAGGCC
TCGTCCTCTGGGTAGAAATCTTTTCGGAATCACTCCGACAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGAACTCGGCTGTCTCTTAATCATT
TAGTAAACCAAGAGCCAAATGCAATGAGTTTCTGCTGACTGTAGTCTTAGCAGGAGGTT
CTTTTGAAGACAGGAAATGGCCCCCTTCTGCTTCTCTTTTTTTTTTTGGAGACAGAGTCT
GCTCTGTTGCCAGGCTGGAGTGCAATGACATGCTCGGCTCTACCCGCAACCTCCGCTC
CTGGGTTCAAGCATTTCTTGCTCTCAGCTCCCTCTAAGTATCTGGGATACAGGCATGTGCCA
CCACACTGGGTGATTTTGTATTTTGTAGTAGAGACGGGTTTACCATGTTGGTTCAGGCTG
GTCTCAAATCTGACCTAGTGATCCACCTCTCGGCTCCCAAGTGCTGGGATACAGG
CATGAGCCACCAAGCTGGCCCCCTTCTGTTTTTGTGTTTGTAGAGAGGAATGAAGTG
GTATGAAGATTAATAAGTATAATTGGCATATAAATTTCAAATTTCAACTGGCTTTTATGCAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATCTGGTTCAGATATAATCAAC
TGTTTATATCAATTTCTAATGATTGCTTTCTTTTATATGGATTCTTTTAAACTTATT
CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTGTACTCAA

CLASS	SUBCLASS
DRAFTSMAN	

253460

1

1

1

FIGURE 33

APPROVED	BY	DATE
CLASS	SUBCLASS	
DRAFTSMAN		

10-10-50

GCGGCACCTGGAAGATGCGCCCATGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
 GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
 GTCCAGTGTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC
 CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
 CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTTATGGG
 AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAGTGGGA
 ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
 TTTATTCAGAGTGTCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
 AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
 TGAAATTCAGGTCTAGCTGGGTATTTATTCAGCAAAAGGCTTGGAATCCCTTCCGAAAT
 CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCGGCTGGCCTGCAGA
 GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGTCAGGGTCTGAGTAAAT
 GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
 GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTGCTAGTTGTATCA
 AATCTGGTACGCAGTATTTTATACCAGTATTTATGTAGTGAAGATGTCAATTAGCAGGA
 AACTAAAATGAATGGAAATCTTAAAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

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RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVITYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEQIEGCIPIKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125